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14. ABSTRACT

In the past one year, we have successfully obtained the DNA samples and epidemiologic questionnaire data as well as setting up the genotyping assays. So far, we have DNA samples from 1200 cases (600 CAs and 600 AAs) and 1200 healthy controls (600 CAs and 600 AAs). The first batch of genotyping is in the process.

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INTRODUCTION

In current proposal, we propos e to conduct a m olecular-based case-control study to evaluate the genetic polym orphisms in selected m iRNA ge nes, responsive elem ents in target genes, and m iRNA processing genes as predictors of breast cancer risk. The study population will consist of 1000 breast cancer pati ents and 1000 healthy controls. W e will also plan to screen germ -line m utations in selected m iRNA genes in 120 AA breast cancer patients who are diagnos ed at early age and have a ggressive diseases with poor prognosis. The proposed research will utilize bi ological specimens and epidem iological data from breast cancer patients and healthy controls sy stematically c ollected by an existing stu dy. W e will integrate epidem iologic and clinical data with the genetic data from the studies. In f urther exp loratory ana lysis, we will evalua te whether SNPs in miRNA genes th at are p redicted to regulate ke y breast can cer genes, SNPs in responsive elements in these key genes, and haplotypes in m iRNA processing genes (*Drosha*, *Dicer*, *DGCR8*, *XPO5*, *TRBP* and *AGO2*) are associated with early age at diagnosis and aggressive disease characteris tics (high-gr ade tum ors and ER-negative status) in AA women.

BODY

In the past one year, we have successfully obtained the DNA sam ples and epidem iologic questionnaire data as w ell as setting up the genotyping assa ys. So far, we have DNA samples from 1200 cas es (600 CAs and 600 AA s) and 1200 healthy controls (600 CAs and 600 AAs). The first batch of genotyping is in the process. This batch will include 124 SNPs proposed in the study, nam ely 57 SN Ps in m iRNA genes and 67 tagSNPs in miRNA processing genes. The pre-tests for all the SNP analyses have bben completed.

KEY RESEARCH ACCOMPLISHMENTS

We have successfully obtained the DNA samples and epidemiologic questionnaire data as well as setting up the genotyping assays. So far, we have DNA samples from 1200 cases (600 CAs and 600 AAs) and 1200 healthy controls (600 CAs and 600 AAs).

124 SNPs proposed in the study, namely 57 SNPs in miRNA genes and 67 tagSNPs in miRNA processing genes, are in the process of genotyping. The pre-tests for all the SNP analyses have bben completed.

REPORT OUTCOME

Due to the nature of the study, we haven't produced the data yet. No significant outcomes are reported at this time.

CONCLUSIONS

So far, the study moves smoothly. We don't expect any problems at current stage. We expect to have ample data to report in second year.